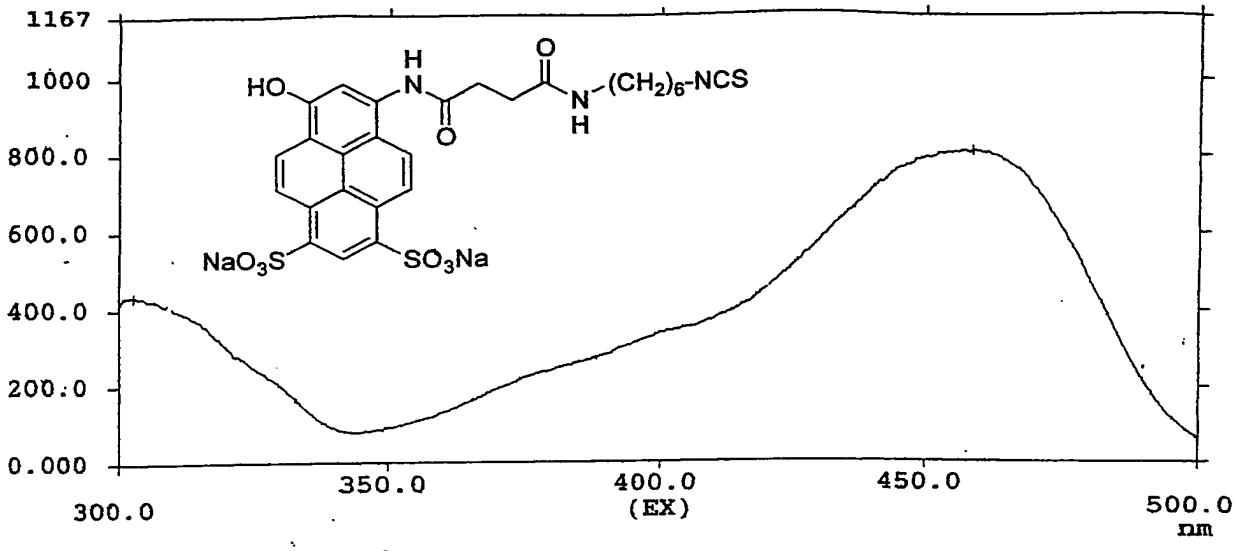
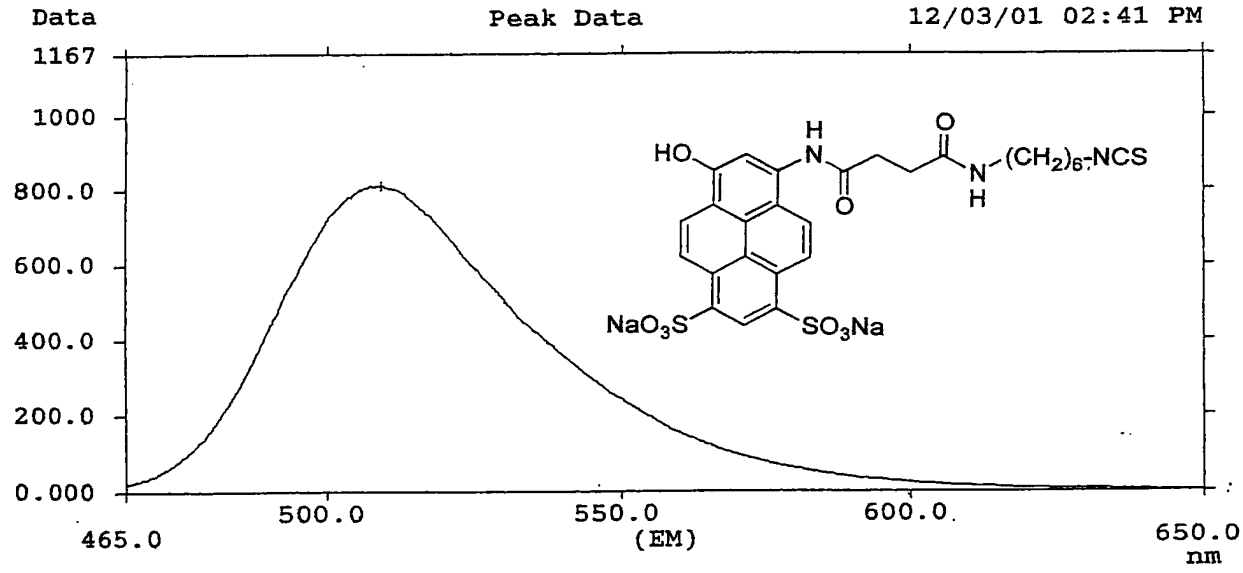
Fig. 1A



Sample : ABC-558-59
Comment : SB Susb.dil pH 9.0
EM : 508.0 nm
Data Mode : Fluorescence
Scan Speed : 1200 nm/min Slit (EX/EM) : 2.5 nm / 2.5 nm
PMT Voltage : 700 V Response : Auto

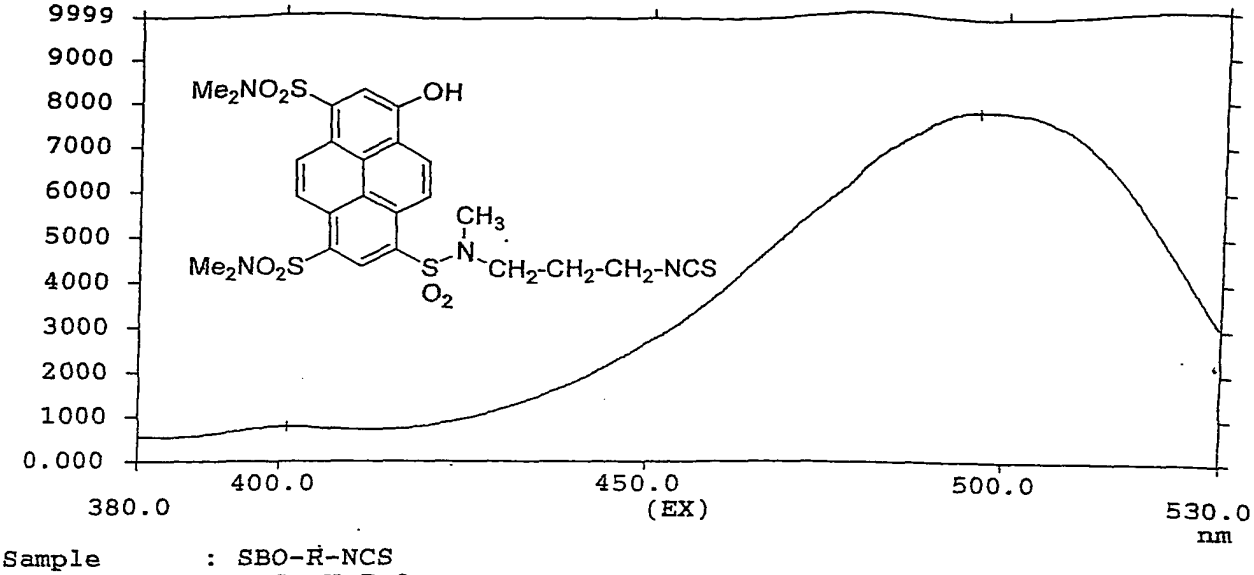
No.	WL (nm)	Peak	No.	WL (nm)	Peak
1	302.6	435.3	2	458.6	811.9



Sample : ABC-558-59
Comment : SB Susb.dil pH 9.0
EX : 458.0 nm
Data Mode : Fluorescence
Scan Speed : 1200 nm/min Slit (EX/EM) : 2.5 nm / 2.5 nm
PMT Voltage : 700 V Response : Auto

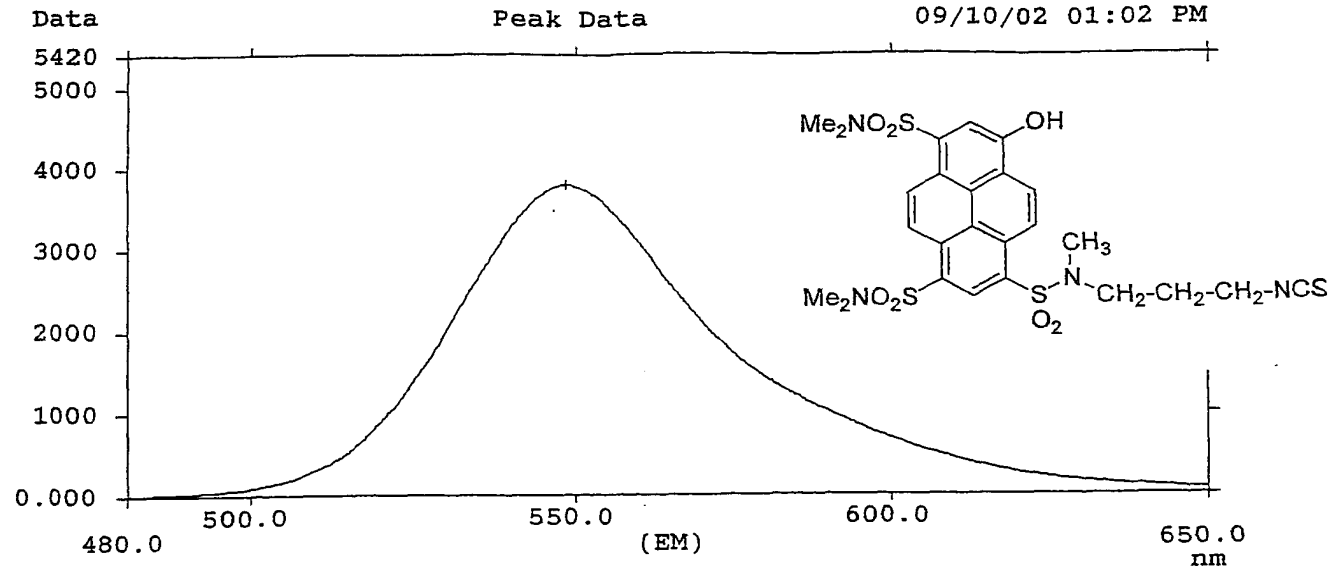
No.	WL (nm)	Peak	No.	WL (nm)	Peak
1	509.0	813.4			

Fig. 1B



Sample : SBO-R-NCS
Comment : PBS pH 7.0
EM : 547.0 nm
Data Mode : Fluorescence
Scan Speed : 1200 nm/min Slit (EX/EM) : 5.0 nm / 5.0 nm
PMT Voltage : 700 V Response : Auto

No.	WL (nm)	Peak	No.	WL (nm)	Peak
1	401.0	783.5	2	496.2	7881



Sample : SBO-R-NCS
Comment : PBS pH 7.0
EX : 460.0 nm
Data Mode : Fluorescence
Scan Speed : 1200 nm/min Slit (EX/EM) : 5.0 nm / 5.0 nm
PMT Voltage : 700 V Response : Auto

No.	WL (nm)	Peak	No.	WL (nm)	Peak
1	548.4	3807			

Fig. 2

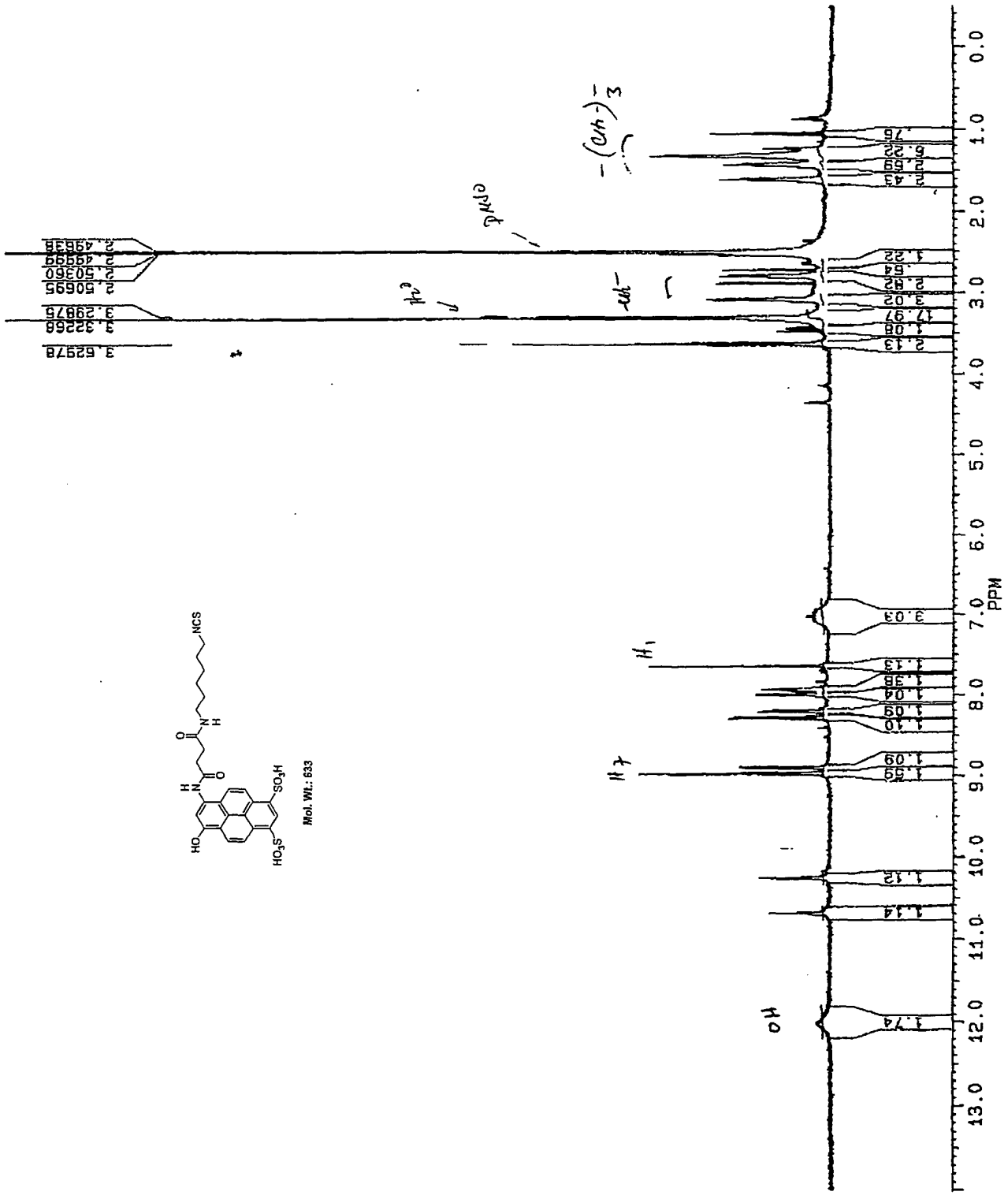


Fig. 3

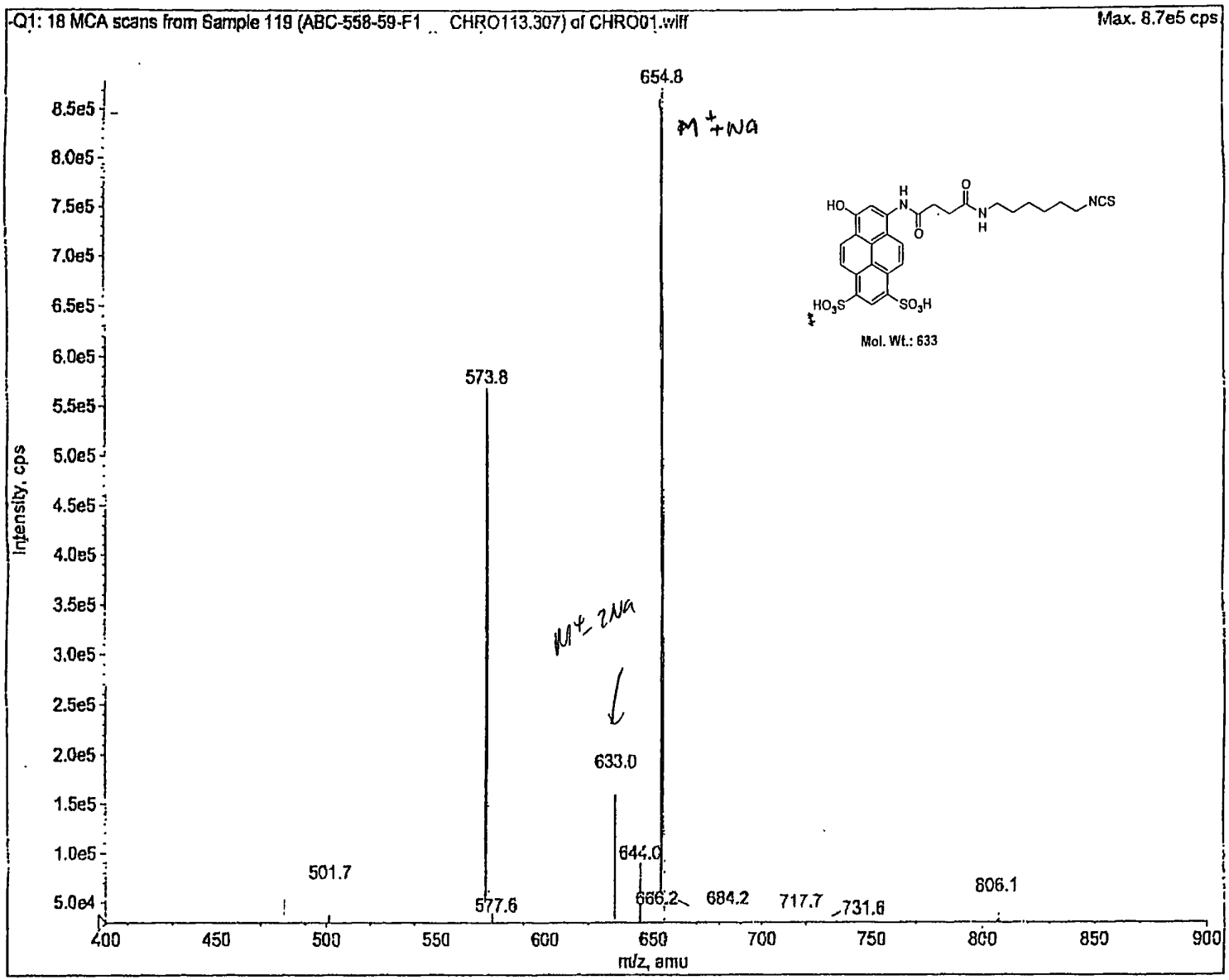

Q1: 18 MCA scans from Sample 119 (ABC-558-59-F1 .. CHRO113.307) of CHRO01.wiff
Max. 8.7e5 cps
654.8
M+Na
573.8
M+2Na
633.0
644.0
501.7
577.6
666.2
684.2
717.7
731.6
806.1
Intensity, cps
m/z, amu
Mol. Wt.: 633

Fig. 4

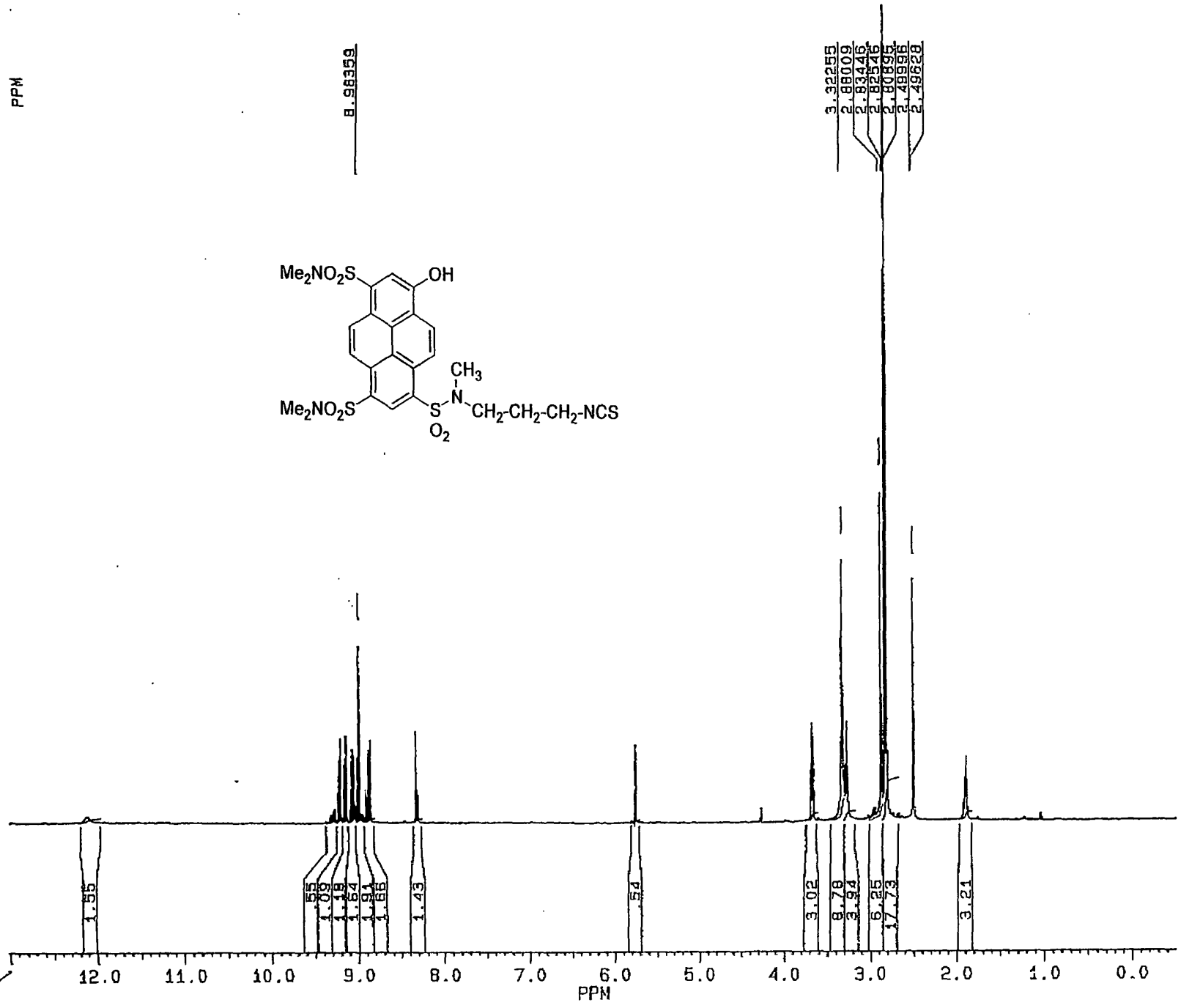
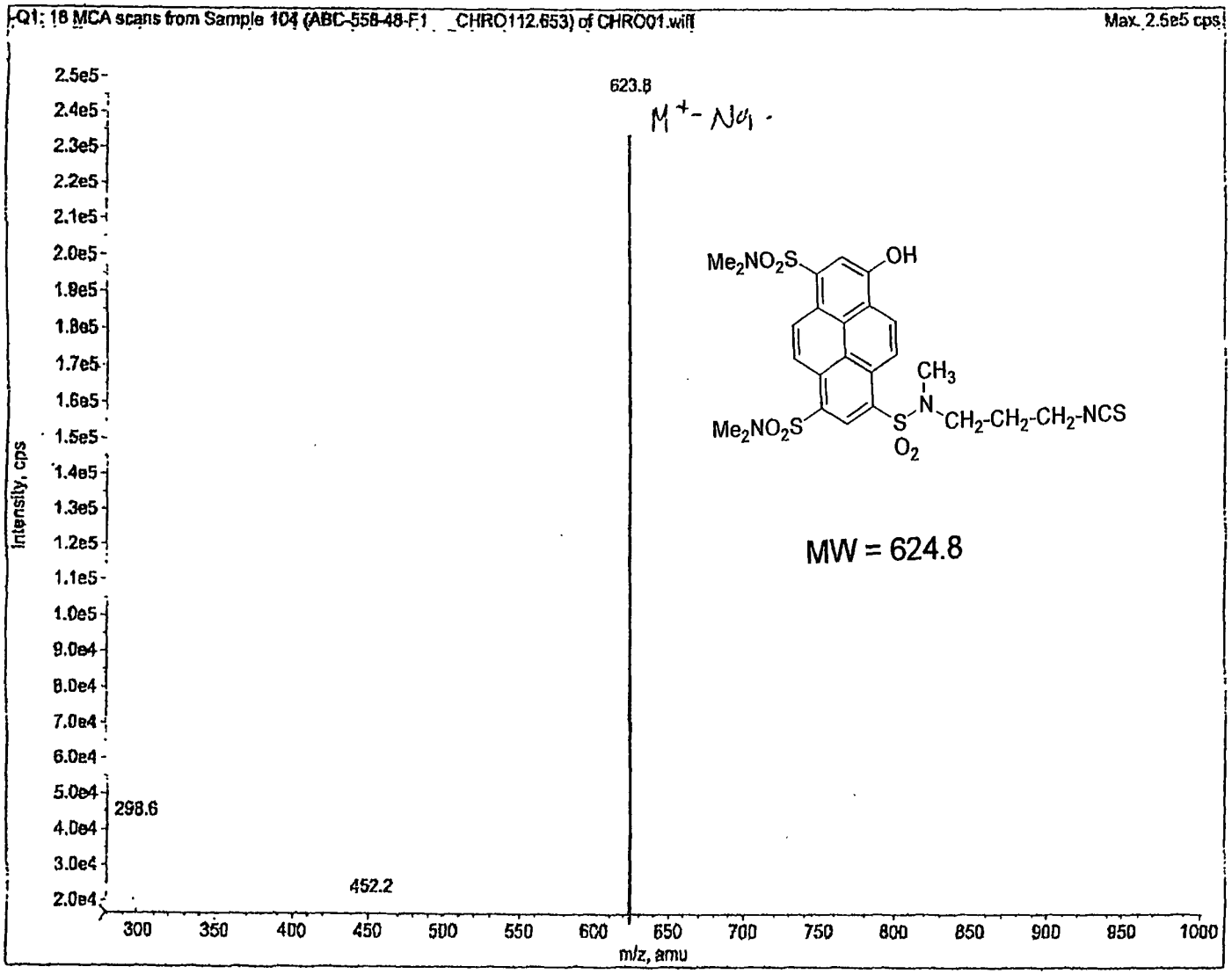

PPM
8.98359
3.32255
2.88009
2.83446
2.82546
2.80895
2.49956
2.49620
Me2NO2S
OH
CH3
N
Me2NO2S
S
O2
CH2-CH2-CH2-NCS
1.55
1.55
1.09
1.48
1.64
1.91
1.66
1.43
.54
3.02
8.78
3.94
6.25
17.73
3.21
12.0
11.0
10.0
9.0
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
PPM

Fig. 5


Q1: 18 MCA scans from Sample 104 (ABC-558-48-F1 _CHRO112.653) of CHRO01.wiff
Max. 2.5e5 cps.
623.8
M+ - Na
Me2NO2S
OH
CH3
N
CH2-CH2-CH2-NCS
Me2NO2S
S
O2
MW = 624.8
298.6
452.2
Intensity, cps
m/z, amu

	NAME	CHAN	LEV	REP	TYPE	DIRECTORY		TIME	DATE
COLLECTION DATA	59693F1	A	1	1	Orig	C:\GOLD\ABC\SAMPLE\	INJECTION	08:53:15	6 MAY 2002
METHOD	PEPY-PEV					C:\GOLD\ABC\METHOD\	ANALYSIS	09:11:24	6 MAY 2002
							REPORT	09:41:26	6 MAY 2002

SAMPLE TABLE 61901CRT C:\GOLD\CERTIFICATE\

SYSTEM 1: SYSTEM1

Chart Speed 0.50 cm/min

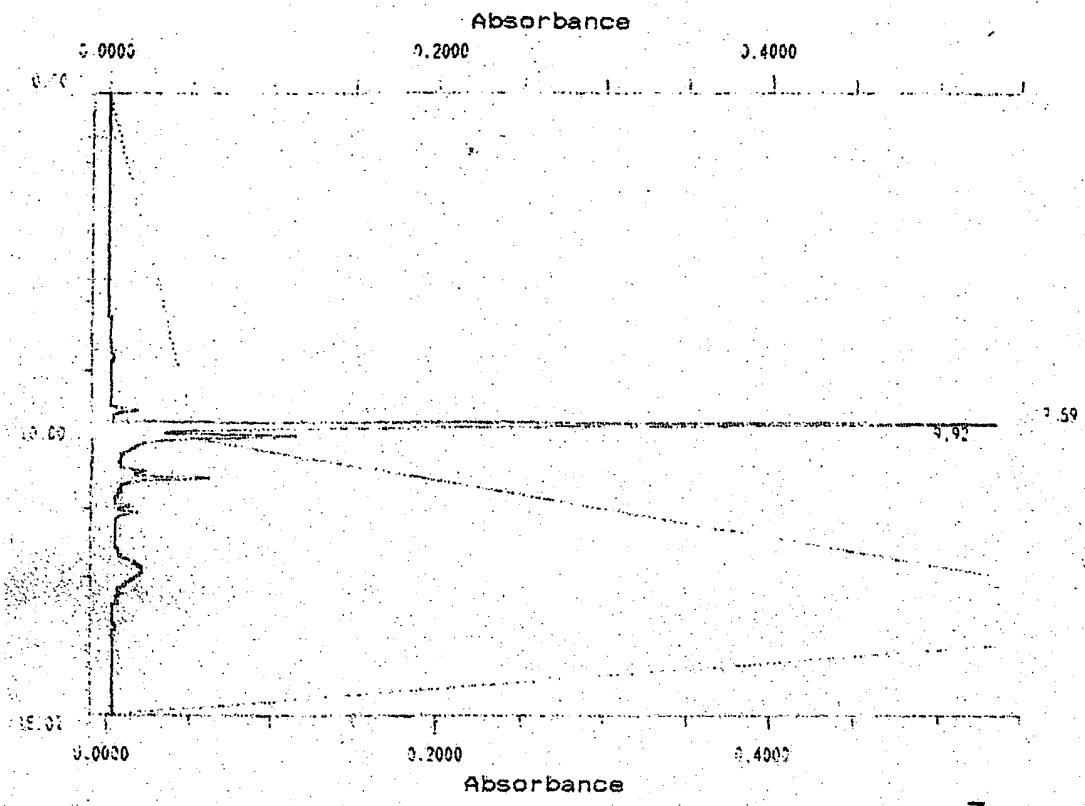
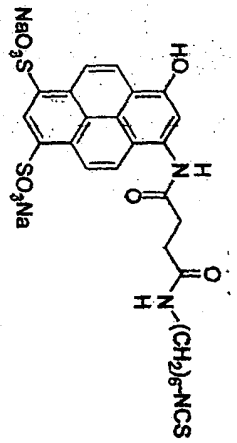


Fig. 6A



	NAME	CHAN	LEV	REP	TYPE	DIRECTORY
COLLECTION DATA	SBOITC96	A	1	1	Orig	C:\GOLD\ABC\SAMPLE\
METHOD	RAM'S					C:\GOLD\ABC\METHOD\

	TIME	DATE
INJECTION	10:18:12	7 AUG 2002
ANALYSIS	10:44:22	7 AUG 2002
REPORT	10:44:25	7 AUG 2002

SAMPLE TABLE 61901CRT C:\GOLD\CERTIFY\CERTIFY
SYSTEM 1: SYSTEM1

Chart Speed 0.50 cm/min

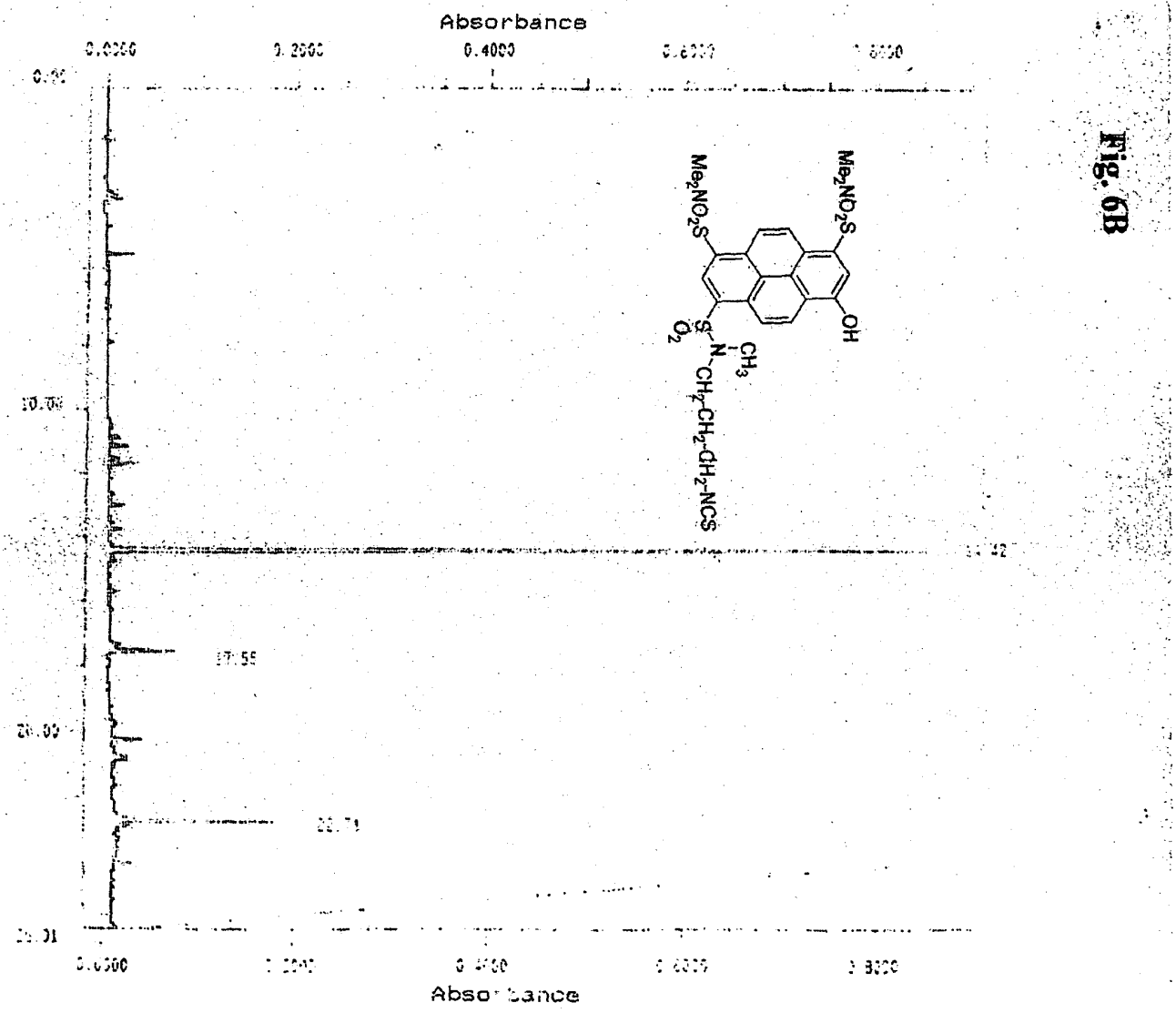
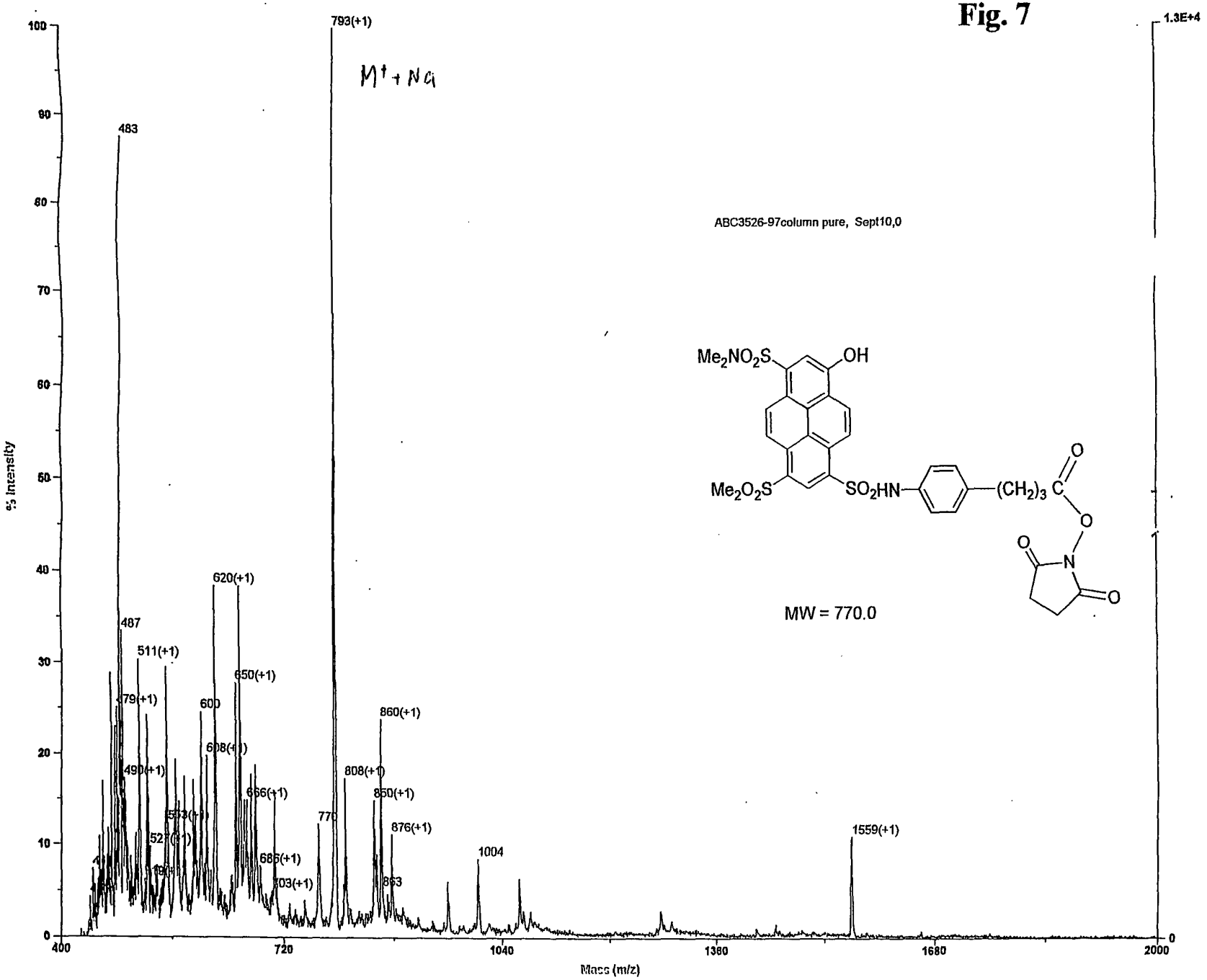


Fig. 6B

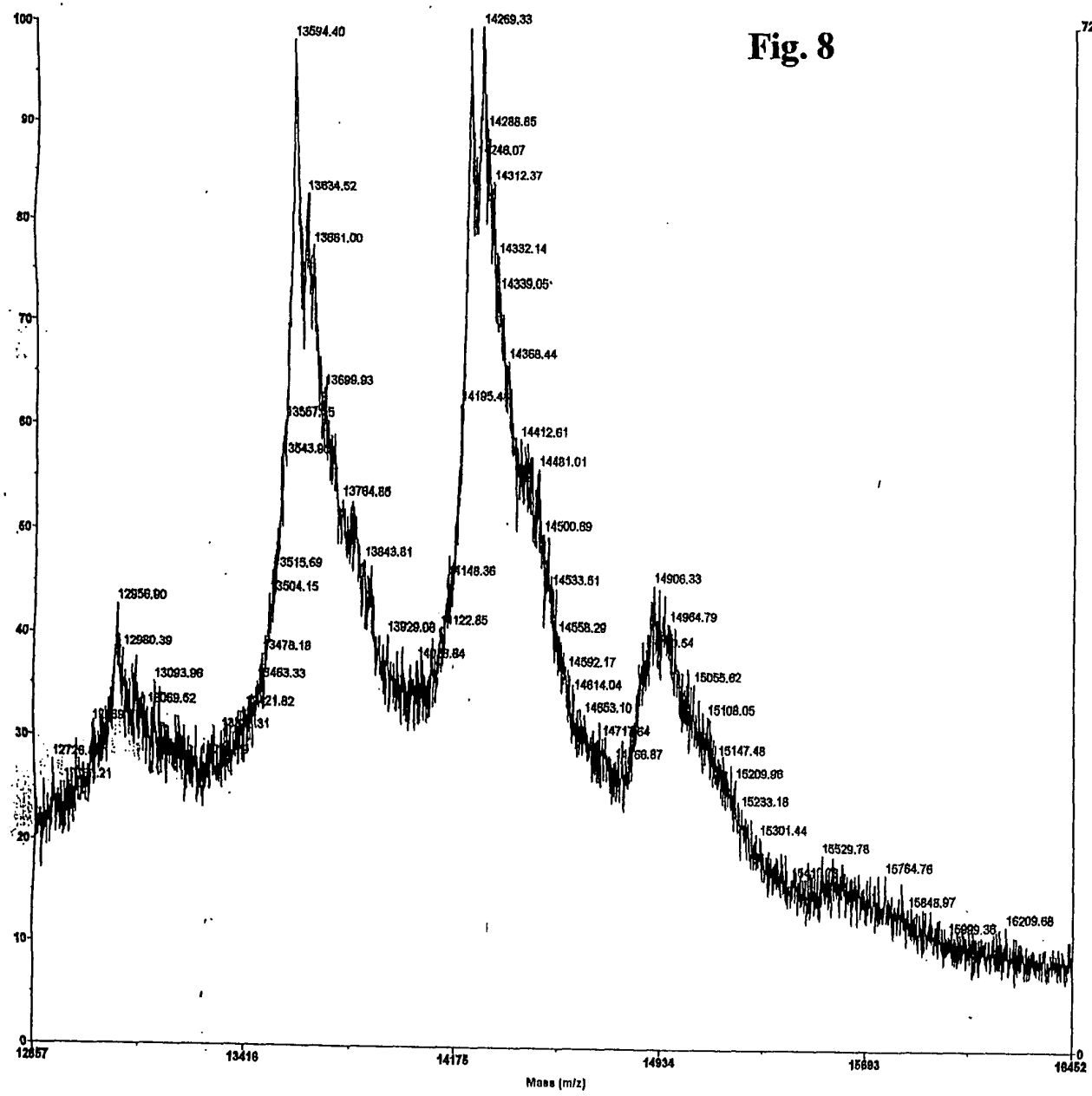
Current Spectrum - 100 shots

Fig. 7



MW = 770.0

Fig. 8



Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
Accelerating voltage:	25000 V
Grid voltage:	93%
Guide wire 0:	0.15%
Extraction delay time:	350 nsec
Acquisition mass range:	7500 – 25000 Da
Number of laser shots:	50/spectrum
Laser intensity:	2617
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	Sinapinic acid
Low mass gate:	7500 Da
Digitizer start time:	48.918
Bin size:	2 nsec
Number of data points:	20113
Vertical scale:	200 mV
Vertical offset:	0.2%
Input bandwidth:	150 MHz
Sample well:	10
Plate ID:	1
Serial number:	1197
Instrument name:	Voyager-DE
Plate type filename:	C:\VOYAGER\100 well plate.plt
Lab name:	PE Biosystems
Absolute x-position:	47487.8
Absolute y-position:	47081
Relative x-position:	180.288
Relative y-posititon:	-226.471
Shots in spectrum:	50
Source pressure:	3.19e-007
Mirror pressure:	0
TC2 pressure:	0.01037
TIS gate width:	30
TIS flight length:	940

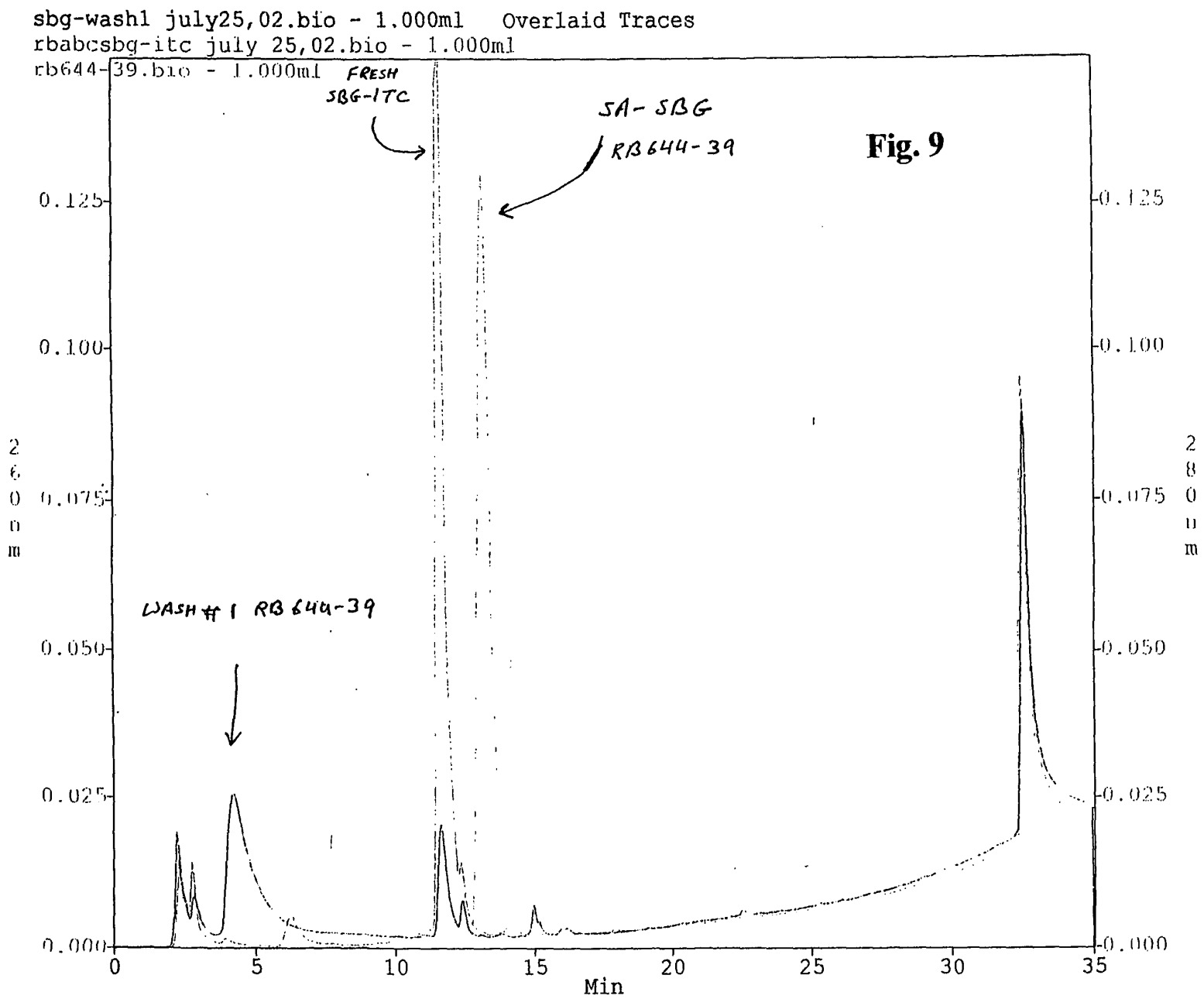
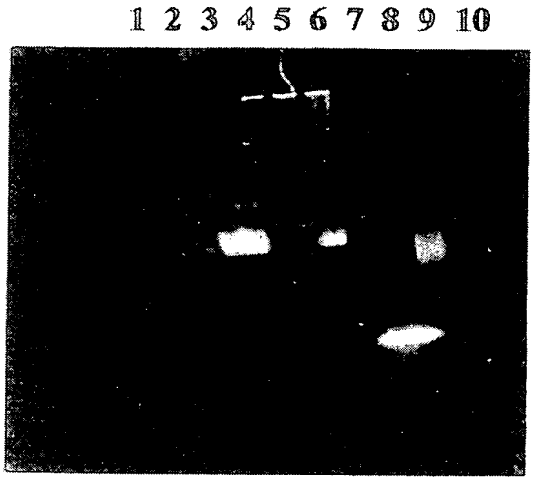

sbg-wash1 july25,02.bio - 1.000ml Overlaid Traces
rbabcsbg-itc july 25,02.bio - 1.000ml
rb644-39.bio - 1.000ml
FRESH SBG-ITC
SA-SBG RB644-39
WASH #1 RB644-39
0.125
0.100
0.075
0.050
0.025
0.000
280 nm
0
5
10
15
20
25
30
35
Min

Fig. 9

Fig. 10

Gel Shift Assay of SA-SBG conjugate:



Lanes:

1 SA ; 5 µg

2 SA-SBG ; 1µg

3 SA-SBG; 5µg

4 SA-SBG ; 10 µg

5 SA-SBG ; 10 µg + Biotin-IgG; 5 µg

6 SA-SBG ; 10 µg + Biotin-IgG; 10 µg

7 SA-SBG ; 10 µg + Biotin-IgG; 2.5 µg

8 Biotin-IgG ; 1 µg

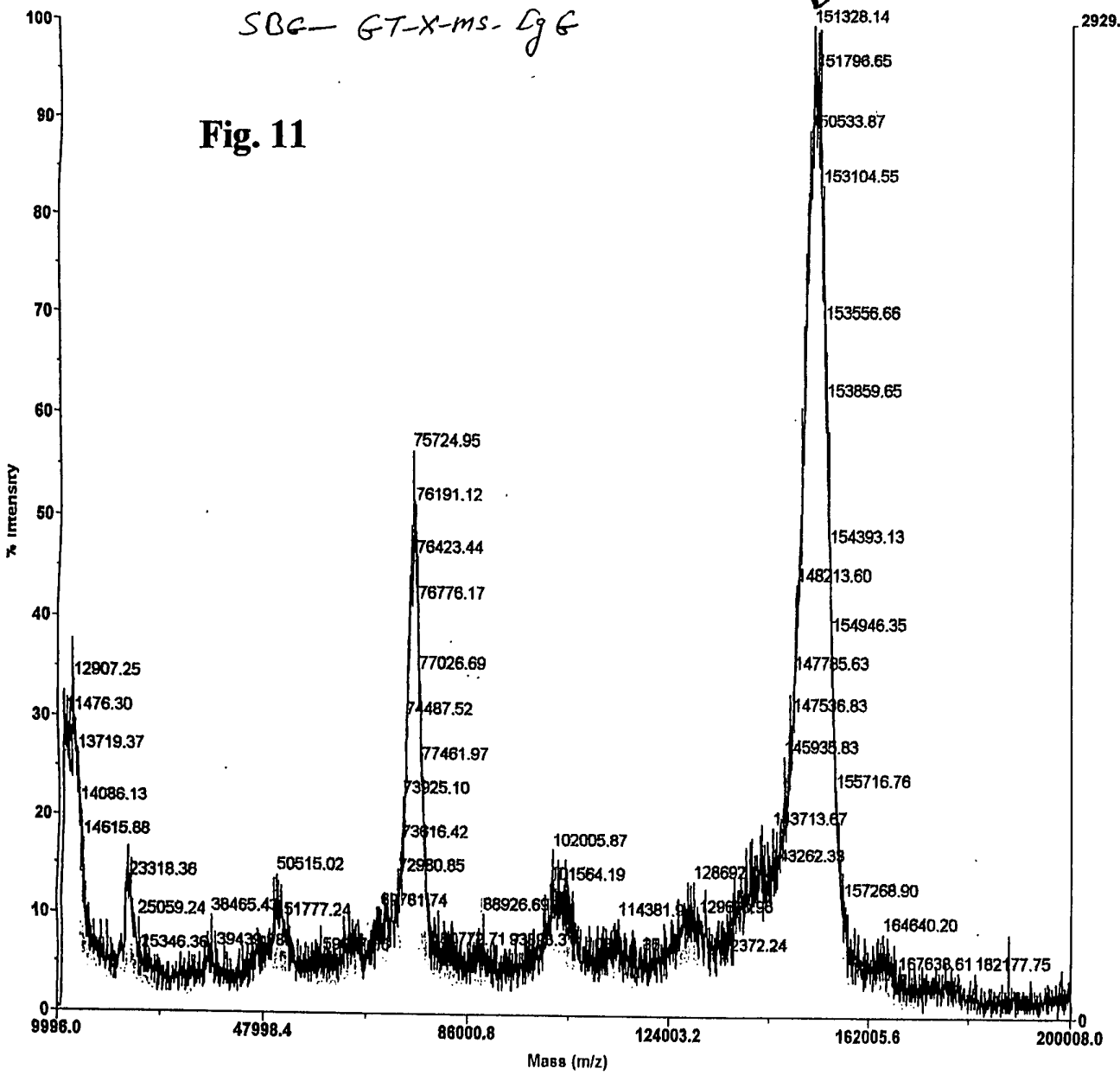
9 SBG ; 1 µg

10 Marker ; 1 µg

SBG— GT-X-ms- IgG

TSBG - GT-X-ms- IgG

Fig. 11



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual

Accelerating voltage: 25000 V
Grid voltage: 93%
Guide wire 0: 0.2%
Extraction delay time: 1700 nsec

Acquisition mass range: 10000 -- 200000 Da
Number of laser shots: 25/spectrum
Laser Intensity: 2817
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration matrix: Sinapinic acid
Low mass gate: 10000 Da

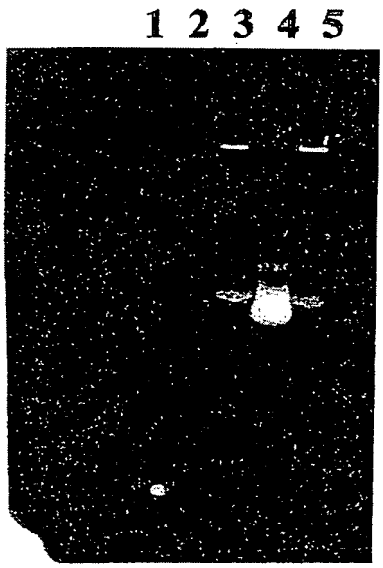
Digitizer start time: 56.65
Bin size: 10 nsec
Number of data points: 19515
Vertical scale: 200 mV
Vertical offset: 0.5%
Input bandwidth: 150 MHz

Sample well: 32
Plate ID: 1
Serial number: 1197
Instrument name: Voyager-DE
Plate type filename: C:\VOYAGER\100 well plate.plt
Lab name: PE Biosystems

Absolute x-position: 7283.04
Absolute y-position: 31932.2
Relative x-position: 615.544
Relative y-position: -135.304
Shots in spectrum: 25
Source pressure: 3.723e-007
Mirror pressure: 0
TC2 pressure: 0.00989
TIS gate width: 30
TIS flight length: 940

Fig. 12

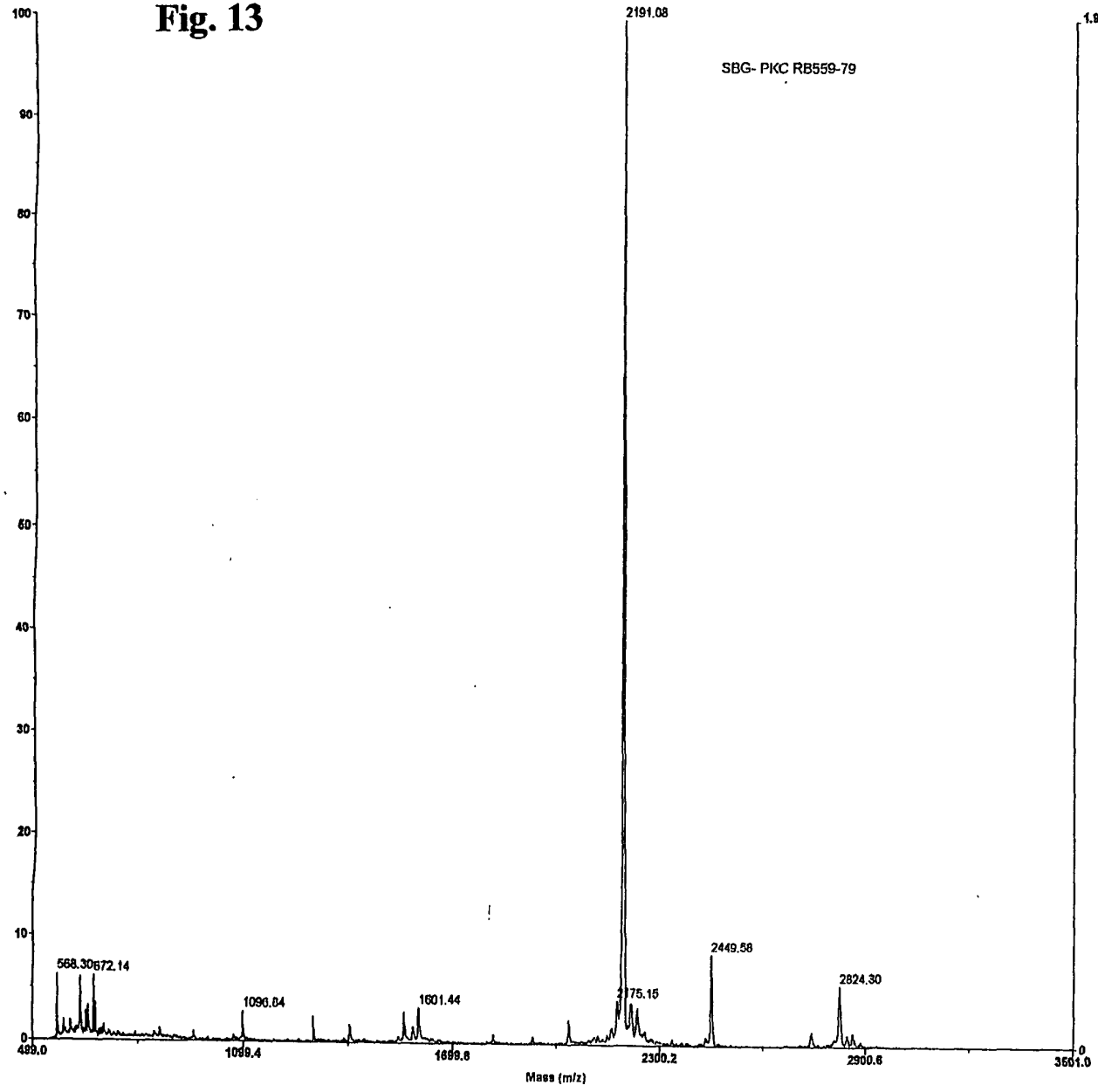
Gel Shift Assay of SA-SBO



Lanes:

1. SA-SBO ; 1 μg
2. SA-SBO + Biotin-IgG ; 5 μg
3. SA-SBO ; 10 μg
4. SA-SBO + Biotin-IgG ; 10 μg
5. Biotin-IgG ; 5 μg

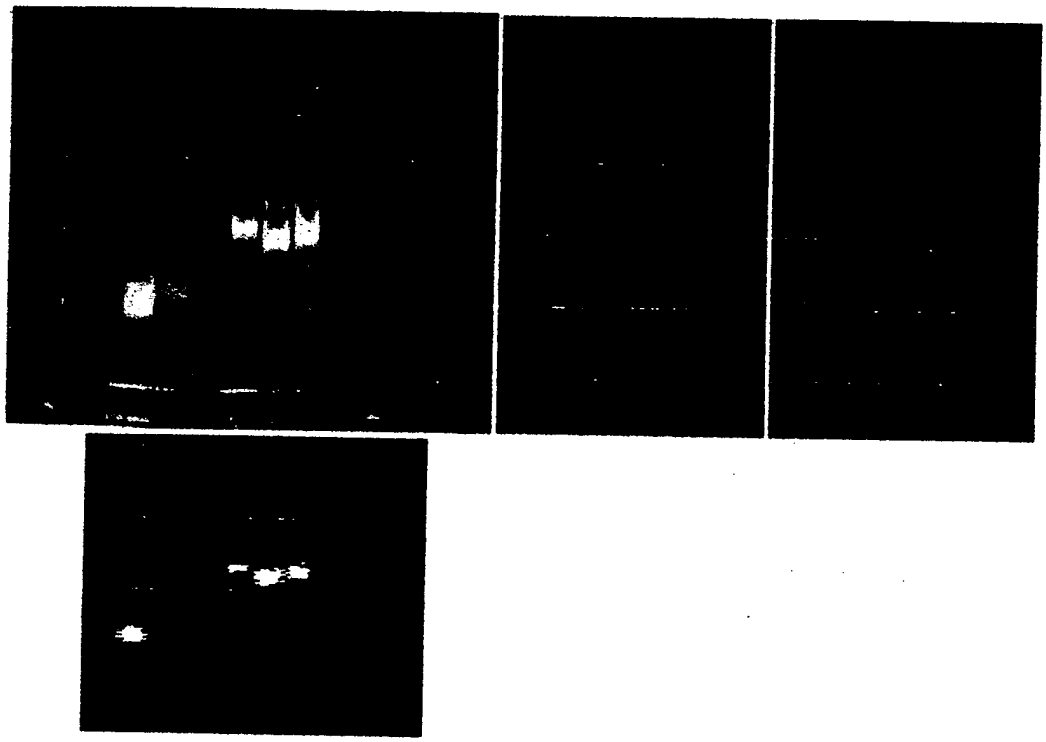
Fig. 13



Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
Accelerating voltage:	20000 V
Grid voltage:	95%
Guide wire 0:	0.05%
Extraction delay time:	200 nsec
Acquisition mass range:	500 -- 3500 Da
Number of laser shots:	100/spectrum
Laser intensity:	1547
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	a-Cyano-4-hydroxycinnamic acid
Low mass gate:	500 Da
Digitizer start time:	14.258
Bin size:	2 nsec
Number of data points:	11636
Vertical scale:	1000 mV
Vertical offset:	0%
Input bandwidth:	150 MHz
Sample well:	21
Plate ID:	1
Serial number:	1197
Instrument name:	Voyager-DE
Plate type filename:	C:\VOYAGER\100 well plate.plt
Lab name:	PE Biosystems
Absolute x-position:	1541.67
Absolute y-position:	37148.1
Relative x-position:	-45.8332
Relative y-posititon:	0.57055
Shots in spectrum:	100
Source pressure:	6.056e-007
Mirror pressure:	0
TC2 pressure:	0.00861
TIS gate width:	30
TIS flight length:	940

POLAROID PHOTOGRAPH

DIGITAL IMAGES
at two thresholds



Digital Image showing
Lane alignment

Figure 14 is a digital image of a polyacrylamide gel showing fluorescent conjugates formed by labeling streptavidin and IgG molecules with the isothiocyanate of StarBright Orange to give labeled reporter moieties having measurable label to probe ratios.

Fig. 15

Figure 15 is a photograph of a polyacrylamide gel showing the fluorescence of an oligonucleotide labeled with StarBright Green Dye.

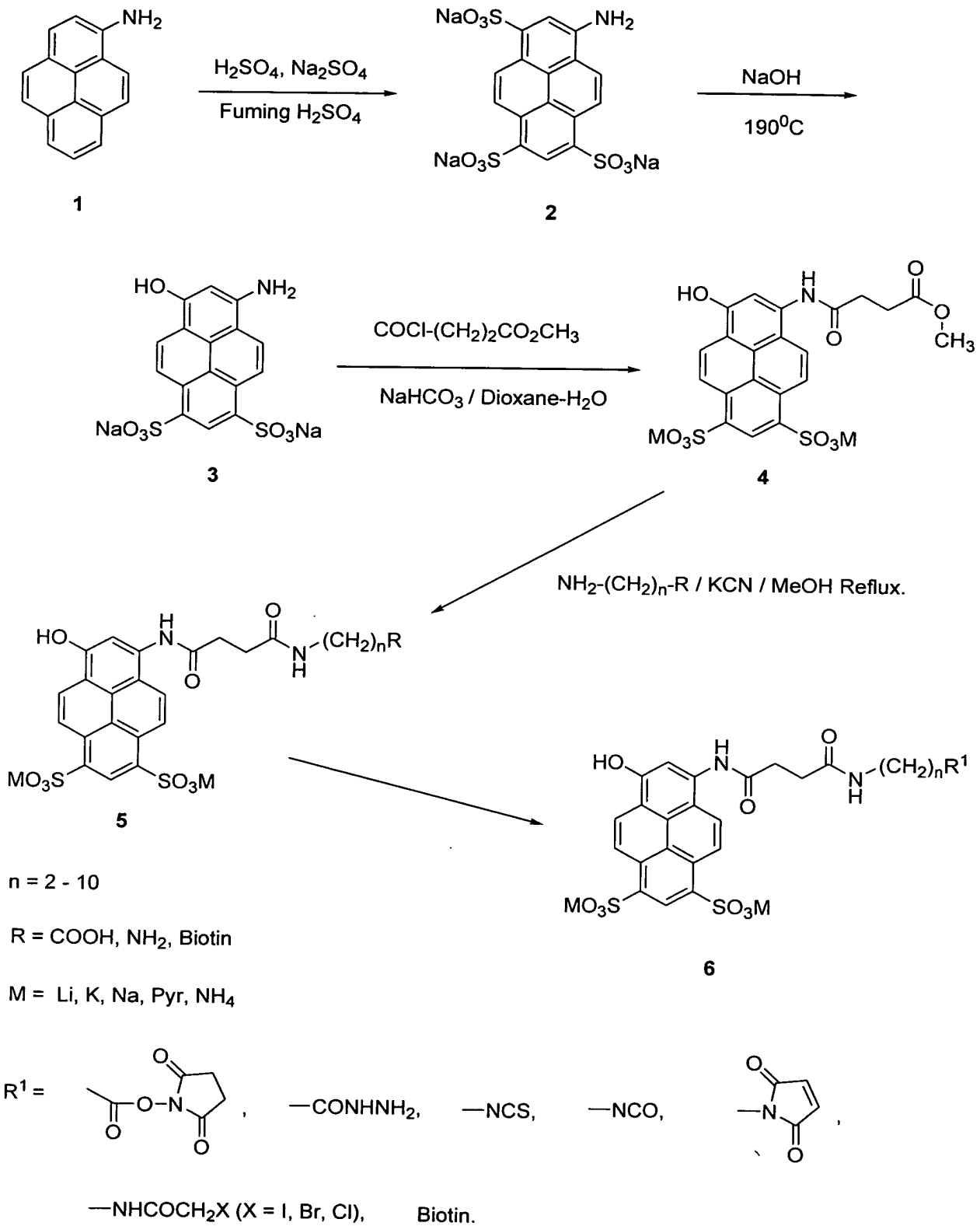
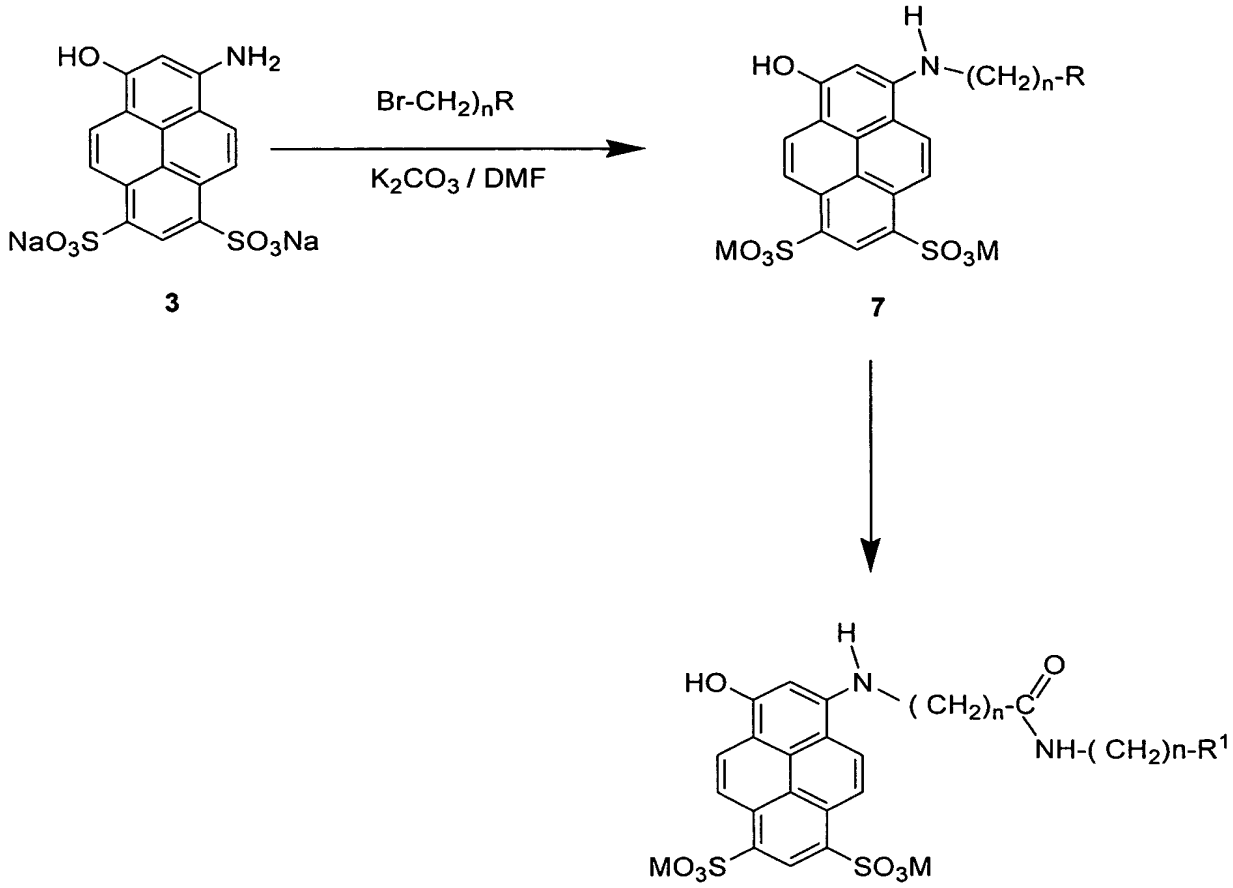

NH2
H2SO4, Na2SO4
Fuming H2SO4
NaO3S
NH2
SO3Na
NaOH
190°C
1
2
HO
COCl-(CH2)2CO2CH3
NaHCO3 / Dioxane-H2O
CH3
MO3S
3
4
NH2-(CH2)n-R / KCN / MeOH Reflux.
(CH2)nR
5
(CH2)nR1
6
n = 2 - 10
R = COOH, NH2, Biotin
M = Li, K, Na, Pyr, NH4
R1 =
—CONHNH2,
—NCS,
—NCO,
—NHCOCH2X (X = I, Br, Cl),
Biotin.

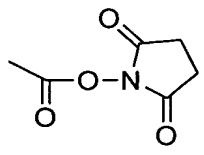
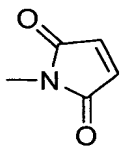
FIG. 16



n = 2 - 10

R = COOH, NH_2, Biotin

M = Li, K, Na, pyr, NH_4

R^1 =  , —$CONHNH_2$, —NCS, —NCO,  ,

—$NHCOCH_2X$ (X = I, Br, Cl), Biotin.

FIG. 17

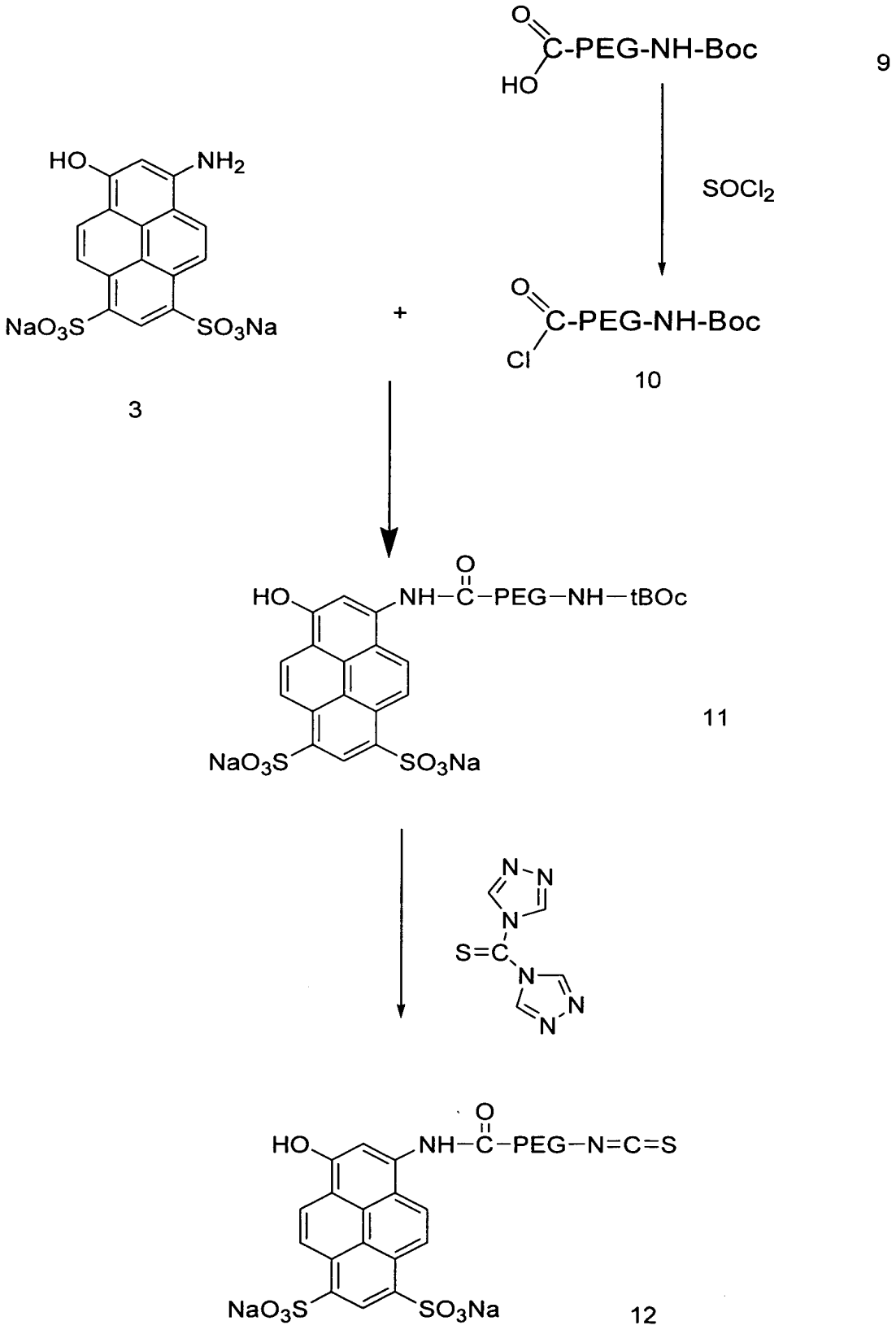
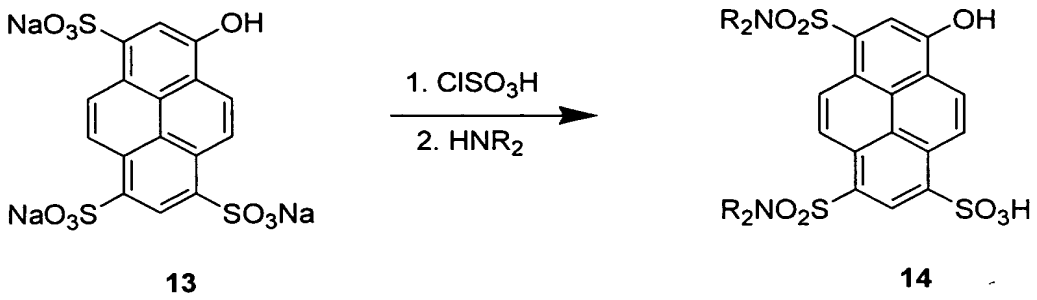
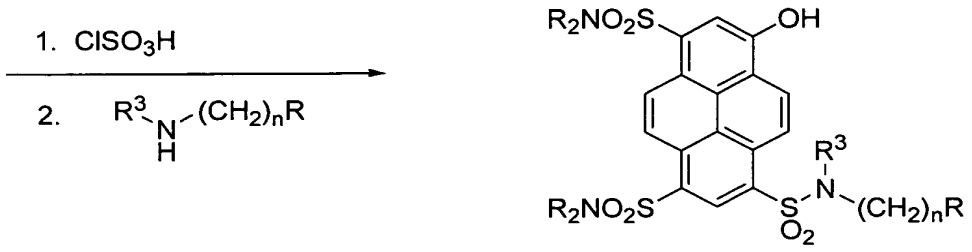

HO
C-PEG-NH-Boc
9
HO
NH2
SOCl2
NaO3S
SO3Na
+
C-PEG-NH-Boc
Cl
10
3
HO
NH–C–PEG–NH–tBOc
11
NaO3S
SO3Na
S=C
HO
NH–C–PEG–N=C=S
NaO3S
SO3Na
12

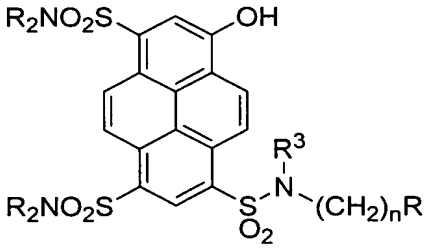
FIG. 18



13 14



15

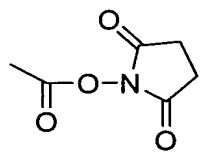
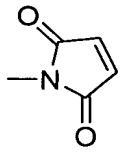


16

n = 2 - 10

R^1, R^2 = alkyl groups

R^3 = H, alkyl groups, R^4 = COOH, NH_2, Biotin

R =  , —$CONHNH_2$, —NCS, —NCO,  ,

—$NHCOCH_2X$ (X = I, Br, Cl), Biotin

FIG. 19

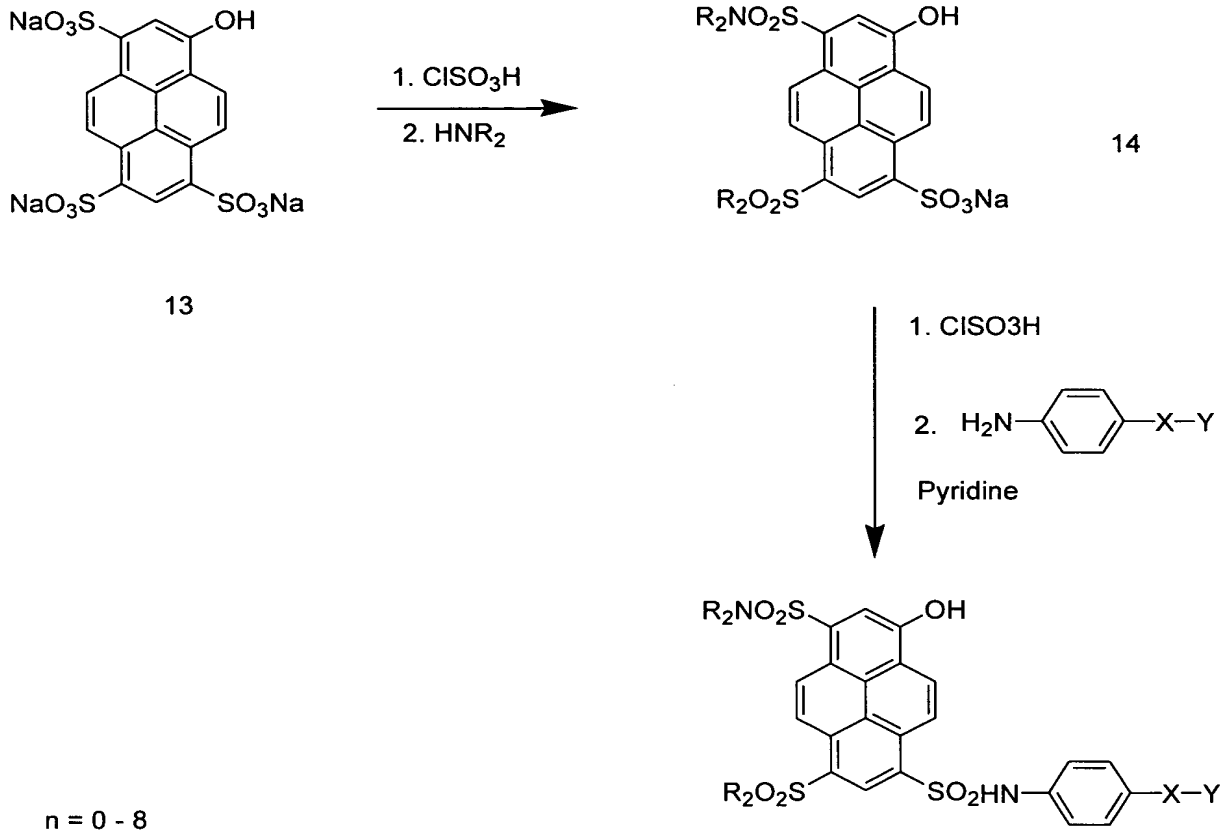

NaO3S
OH
NaO3S
SO3Na
1. ClSO3H
2. HNR2
R2NO2S
OH
R2O2S
SO3Na
14
13
1. ClSO3H
2. H2N
X—Y
Pyridine
R2NO2S
OH
R2O2S
SO2HN
X—Y
17
n = 0 - 8
R = Alkyl groups
X = - (CH2)n-
X = COOH,
—CONHNH2,
—NCS,
—NCO,
—NHCOCH2X (X = I, Br, Cl), Biotin

FIG. 20

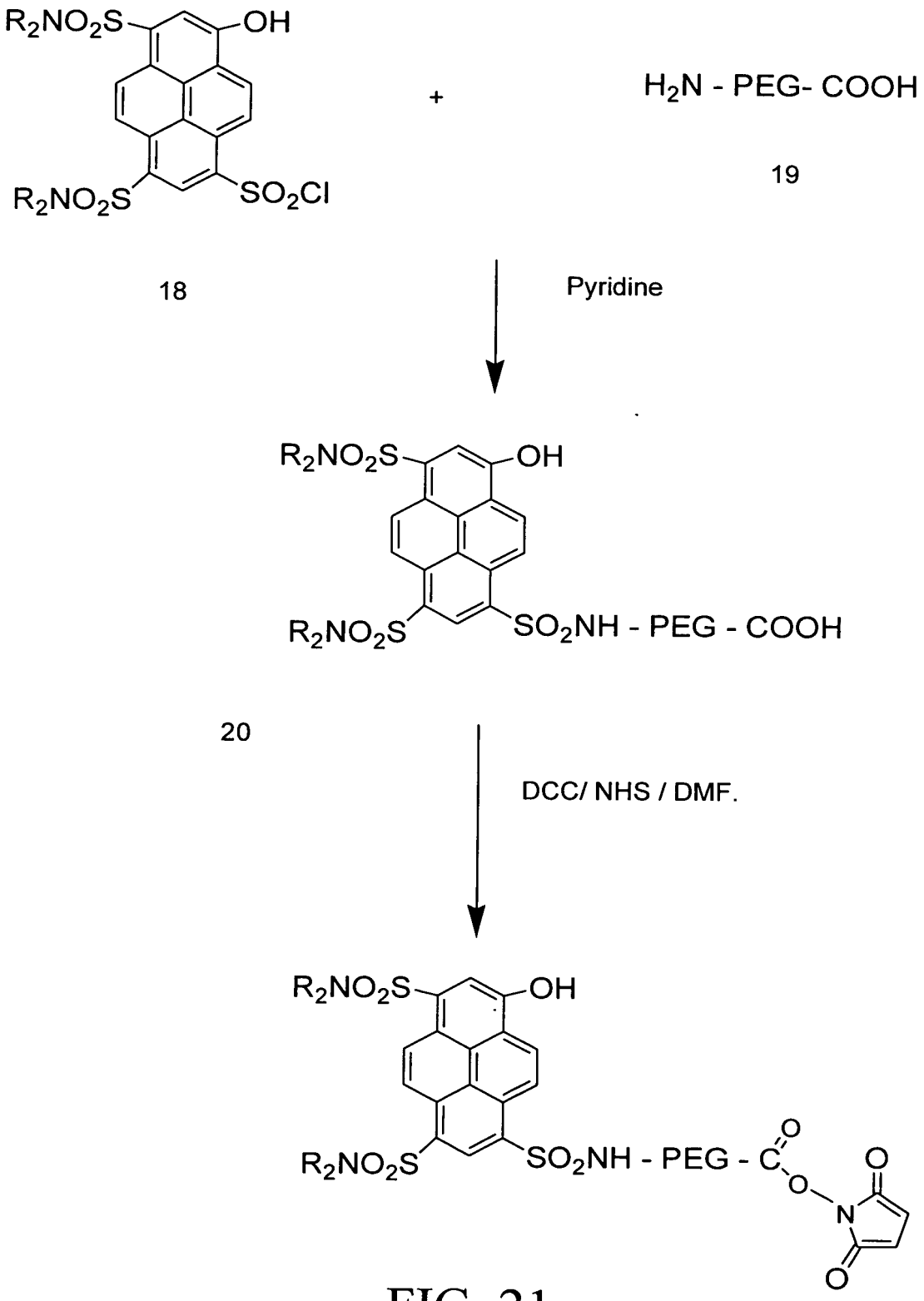

R2NO2S
OH
R2NO2S
SO2Cl
18
+
H2N - PEG- COOH
19
Pyridine
R2NO2S
OH
R2NO2S
SO2NH - PEG - COOH
20
DCC/ NHS / DMF.
R2NO2S
OH
R2NO2S
SO2NH - PEG - C
O
O
N
O
O

FIG. 21